FOKANCSATS

FORANCSATS

hApo420pep

hTRADEbeta_

Consensus

POKANCSATS

DAICGDCLPG

DAICGDCLPG

FYRKTKLVGF

FYRKTKLVGF

FYRKTKLVGF

DAICGDCLPG

PPPPYEPHCA

ODMECVPCGD

ODMECVPCGD

QDMECVPCGD

PPPPYEPHCA

PPPPYEPHCA

Consensus Sequence

	1.00	1.00	1.00	1.00		50	FR DRSGNCVPCN		100	CK PCLDCAVVNR	CK PCLDCAVVNR	CK PCLDCAVVNR	CK PCLDCAVVNR		C	GD PPPPYEPHCA	SONDERPHOR				
ck: 6430	Weight:	Weight:	Weight:	Weight:			SGDCROOEFR	SGDCRQQEFR	TGDCRQQEFR	SCDCROOEFR	SGDCROOEFR			REDWGFORCK	REDWGFORCK	REDWGFORCK	* KEDWGFOKCK	KEDWGFOKCK		GDMECVPCGD	ODMECVPCGD
CompCheck:	4050	4128	7937	8173			GYLSCKVTCE	GYLSCKVTCE	GYLSCRVTCE	GYLSCRVTCE	GYLSCKVTCE			QCVTCRLERF	QCVTCRLHRF	QCVTCRLHRF	QCVACRLHRF	QCVTCRLHRF		FYRKTKLVGF	FYRKTKLVGF
blosum62.cmp	423 Check:	423 Check:	423 Check:	423 Check:			KTFFTLLVLL	KTFFTLLVLL	KTFFTLLVLL	KTFFTLLVLL	KTFFTLLVLL			ECGFGYGEDA	ECGFGYGEDA	ECGFGYGEDA	ECGFGYGEDA	ECGFGYGEDA		DAICGDCLPG	DAICGDCLPG
table: <u>b</u>	1 Len:	Len:	1 Len: 4	Len:			MALKVLLEQE P	MALKVLLEQE B	malkvilege b	malkvileoe b	malkvilege b			OCGPGMELSK F	OCGPGMELSK F	OCGPGMELSK F	OCGPGMELSK F	OCGPGMELSK F	-	FOKANCSATS D	FORANCSATS D
comparison	hTRADEalpha	htrain 1	hTRADEbeta	hApo420pep		-	.1	н,	≓,		Consensus Ma	i	16	1	-	H			101	.1	htrain_1 FG
Symbol o	Name: h	Name: h	Name: h	Name: h	>		hTRADEalpha	htrain	hTRADEbeta	рАро420рер	Cons			hTRADEalpha	htrain	hTRADEbeta	hApo420pep	Consensus		nikangalpha	hTRA



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SVQTCGPVRL

HRACCOCRRD

FDRPQLHEYA

IQYNETELSC

KPSWSLRSOD

hApo420pep

Consensus

KPSWSLRSQD

IQYNGSELSC

HRACCOCRRD

FDRPQLHEYA

SVQTCGPVRL

200	IYCKRQFWEK	IYCKRQFWEK	IYCKRQFWEK	IYCKRQFWEK	IYCKRQFMEK	250	SVQTCGPVRL	SVQTCGPVRL	SVQTCGPVRL
	VLLALLILCV IYCKRQFWEK	VLLALLILCV	VLLALLILCV	VLLALLILCV	VLLALLILCV		HRACCOCRRD	HRACCQCRRD	HRACCOCRRD
	AAVICSALAT	AAVICSALAT	AAVICSALAT	AAVICSALAT	AAVICSALAT		FDRPQLHEYA	FDRPQLHEYA	LDRPQLHEYA
	TASSPRDTAL	TASSPRDTAL	TASSPRDTAL	TASSPRDTAL	TASSPRDTAL		IQYNGSELSC	IQYNGSELSC	IQYNGSELSC
151	SKVNLVKIAS TASSPRDTAL	SKVNLVKIAS	SKVNLVKIAS	SKVNLVKIAS	SKVNLVKIAS TASSPRDTAL	201	KPSWSLRSQD	KPSWSLRSQD	KPSWSLRSOD
	hTRADEalpha_	hTRAIN_1	hTRADEbeta_1	hApo420pep	Consensus		hTRADEalpha_	hTRAIN_1	hTRADEbeta_1

	251				300
hTRADEalpha_	LPSWCCEEAC	SPNPATLGCG	VHSAASLQAR	SPNPATLGCG VHSAASLQAR NAGPAGEMVP TFFGSLTQSI	TFFGSLTQSI
hTRAIN_1	LPSWCCEEAC	SPNPATLGCG	VHSAASLQAR	SPNPATLGCG VHSAASLQAR NAGPAGEMVP TFFGSLTQSI	TFFGSLTQSI
hTRADEbeta_1	LPSWCCEEAC	SPNPATLGCG	VHSAASLQAR	SPNPATLGCG VHSAASLQAR NAGPAGEMVP TFFGSLTQSI	TFFGSLTQSI
hApo420pep	LPSWCCEEAC	SPNPATLGCG	SPNPATLGCG VHSAASLQAR NAGPAGEMVP	NAGPAGEMVP	TFFGSLTQSI
Consensus	LPSMCCEEAC	SPNPATLGCG	VHSAASLQAR	SPNPATLGCG VHSAASLQAR NAGPAGEMVP TFFGSLTQSI	TFFGSLTQSI



350 LESSTSLDSN LESSTSLDSN LESSTSLDSN LESSTSLDSN LESSTSLDSN GEDIHSLNPE GEDIHSLNPE GEDIHSLNPE GEDIHSLNPE GEDIHSLNPE SFCDSYPELT SFCDSYPELT SPCDSYPELT SFCDSYPELT SFCDSYPELA MONPMGGDNI MONPEGGDNI MONPEGGDNI MONPMGGDNI MONPMGGDNI CGEFSDAWPL CGEFSDAWPL CGEFSDAWPL CGEFSDAWPL CGEFSDAWPL 301 hApo420pep Consensus hTRADEalpha hTRADEbeta_ hTRAIN

ALTWRSQLDQ ALTWRSQLDQ ALTWRSQLDQ ALTMRSQLDQ ALTWRSQLDQ TLVESASTQD TLVESASTOD TLVESASTQD TLVESASTQD TLVESASTOD AATDLSRYNN AATDLSRYNN AATDLSRYNN AATDLSRYNN AATDLSRYNN PVQSHSENFT PVQSHSENFT PVQSHSENFT PVQSHSENFT PVQSHSENFT SSQDLVGGAV SSODLVGGAV SSODLVGGAV SSQDLVGGAV GAV SSÖDLVG 351 hApo420pep Consensus hTRADEalpha hTRADEbeta_ **h**TRAIN

423 GSL GSL GSL 1 QTSLQVRQRL QTSLQVRQRL QTSLQ--QRL QTSLQEA~~~ QTSLQEA~~ ESGAVIHPAT ESGALIHPAT ESGAIIHPAT ESGAVIHPAT ESGA-IHPAT 401 hApo420pep Consensus hTRADEalpha hTRADEbeta_ **h**TRAIN

COLONIA DE LA CO

FIG. 2

TRADE- α TRADE- β

ESGAIIHPATQTSLQEA
ESGAIIHPATQTSLQVRQRLGSL
I 401 416 423

FIG. 3

CRD1

NGFRp75	CPTGLYT.H SGECCKA	NLGEGVAQPCG.ANQTVCE
OX40	CGDTYPS NDRCCHE	RPGNGMVSRCSRSQNTVCR
CD40	CREKQYL.L NSQCCSL	QPGQKLVSDCTEFTETECL
TRADE	CROQEFRDR SGNCVPCNOC	GPGMELSKEC GFGYGEDAQCV

CRD2

NGFRp75				MSAPCVE	
OX40	PCGPGFY	NDVVSSKPCK	PCTWC.NLRS	GSERKQLCTA	TODTVC
CD40	PCGES.EFL	DTWNRETHCH	OHKYCDPNLG	LRVQQKGTSE	T.DTIC
TRADE	TCRLHR.FK	EDWGFQK.CK	PCLDCAVVN.	.rfqkancsa	TSDAIC

SUBCLASS

100 150 150 100 200 250 250 200 300 350 349 400399 50 50 **QCGPGMELSKECGFGYGEDAQCVTCRLHRFKEDWGFQKCKPCLDCAVVNR** TSDAICGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCA **QCGPGMELSKECGFGYGEDAQCVPCRPHRFKEDWGFQKCKPCADCALVNR** TSDAVCGDCLPGFYRKTKLVGFQDMECVPCGDPPPPYEPHCh SKVNLVKIJASTASSPRDTALAAVICSALATVLLALLILCVİYCKRQFMEK VKI<mark>SSTASSPRDTALAAVICSALATVLLALLILCVIYCKRQFMEK</mark> CEEACSPN PAITLGCCVHSPASL QARNAGPAGEMVPITFFGSLTQSI VPVOSHSENFTAATDLSRYNNTLVESASTODALTMRSOLDO ALESSGNVSESTDSPRHGDTGTVWEDTLAQDADRTPSOGGW CEEARSBARAVLGCGLRSPTTLQERNPASVGDTMPAFFGSVSRSI ESSTSLDSN CDSYPELTGEDTNSINPENESPABLDSS HEYAHRACCOCKRDSVQTCGPVR LRSQDIQYNGSELSCFDQPRLRHCAHRACCQYHRDSAPMYGPVH MALKVLLEQEKTEFTLLVILGYLSCKVTCESGDCRQQEFRDRSGNCV MALKVLPLHRTVLFAAILFLLHLACKVSCEFGDCRQQEFKDRSGNCV DAWPLMONPMGGDNISFCDSYPELTGEDIHSLNPEL LRSQDIQYNGSELSCFORPOL 417 SL GGDS-DAWPLMONPL THEATOTE CSM FOKANCSA LPSMC(IPSLC(CEFE FQKAN SKVNL KPSWS KPSWS CAEFSI SSDDL ESGAV EDREN GGDDL $TRADE\alpha$ $TRADE\alpha$ TRADEα $TRADE\alpha$ TRADEα $TRADE\alpha$ $TRADE\alpha$ $TRADE\alpha$ $TRADE\alpha$ TRADE TRADE TRADE TRADE TRADE TRADE TRADE TRADE TRADE NO: 6MOUSE NO: 2HUMAN NO:2HUMAN NO:2HUMAN NO: 6MOUSE NO:2HUMAN NO: 6MOUSE NO: 6MOUSE NO:2HUMAN NO:2HUMAN NO:2HUMAN NO: 6MOUSE NO:2HUMAN NO: 6MOUSE NO: 6MOUSE NO:2HUMAN NO: 6MOUSE NO: 6MOUSE QI ID ΠD ID ID ID ΠD QH ID ID 01 10 ID ID ID ID SEQ
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FIG. 5A

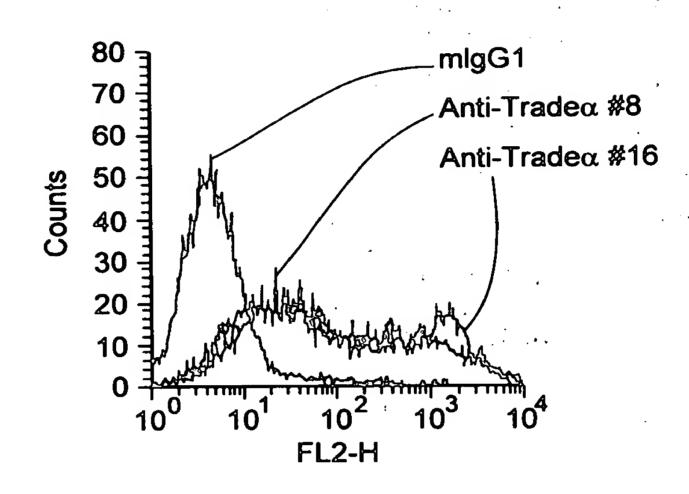


FIG. 5B

FIG. 5C

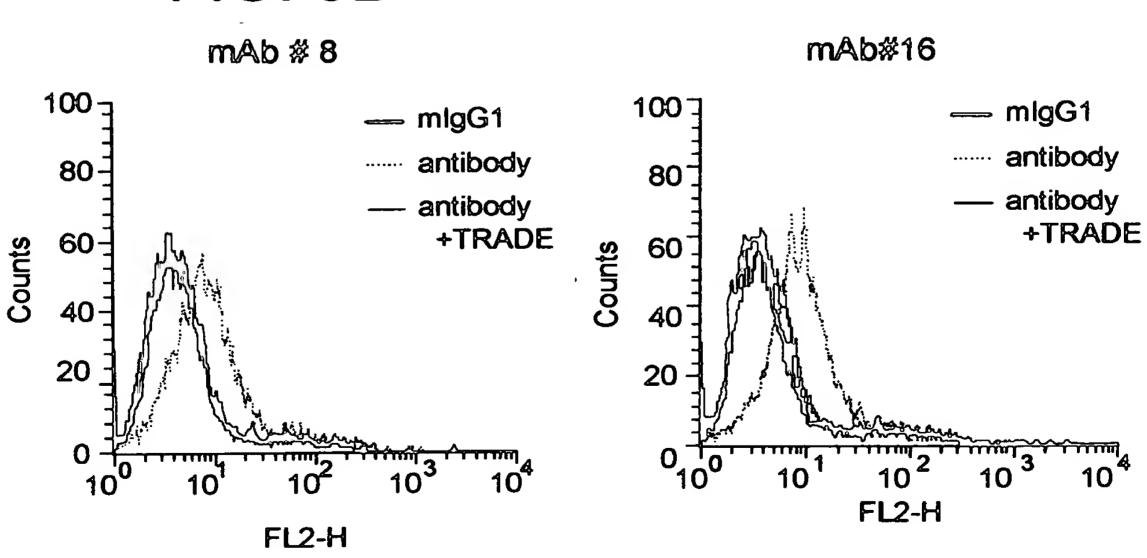


FIG. 6A

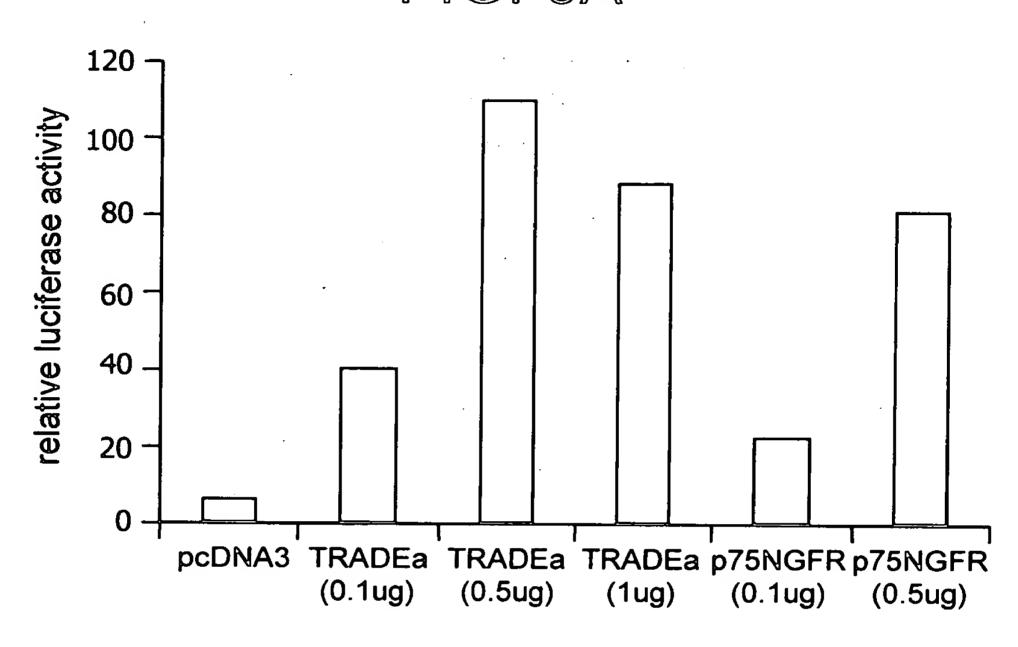
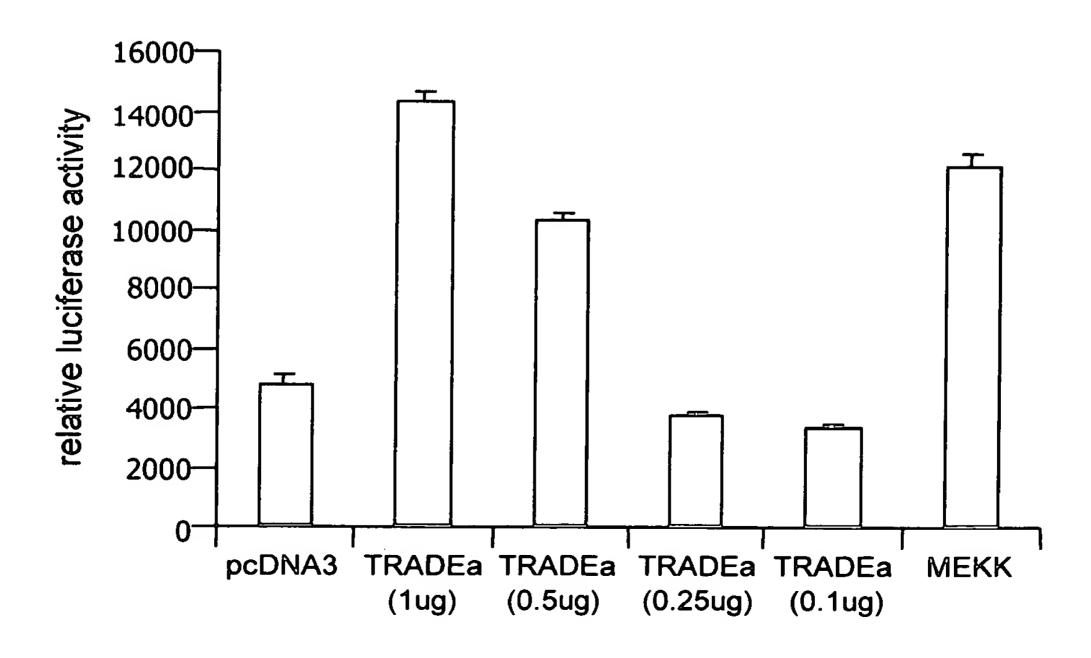
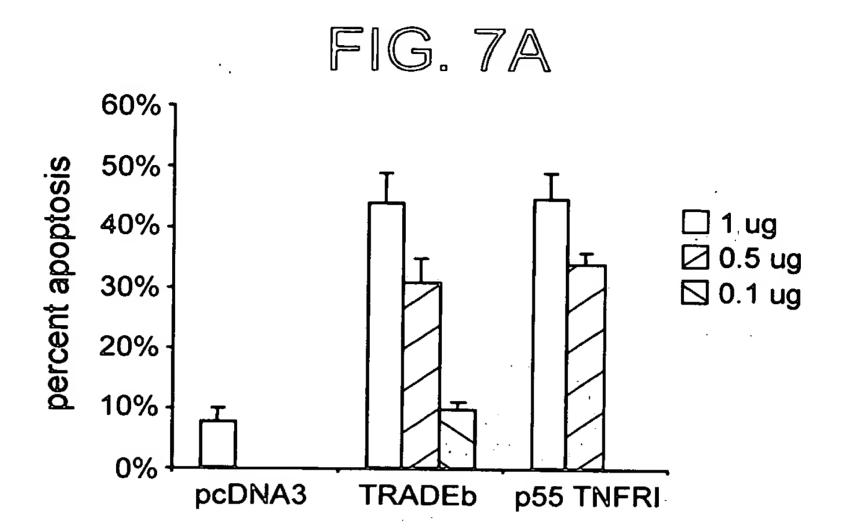


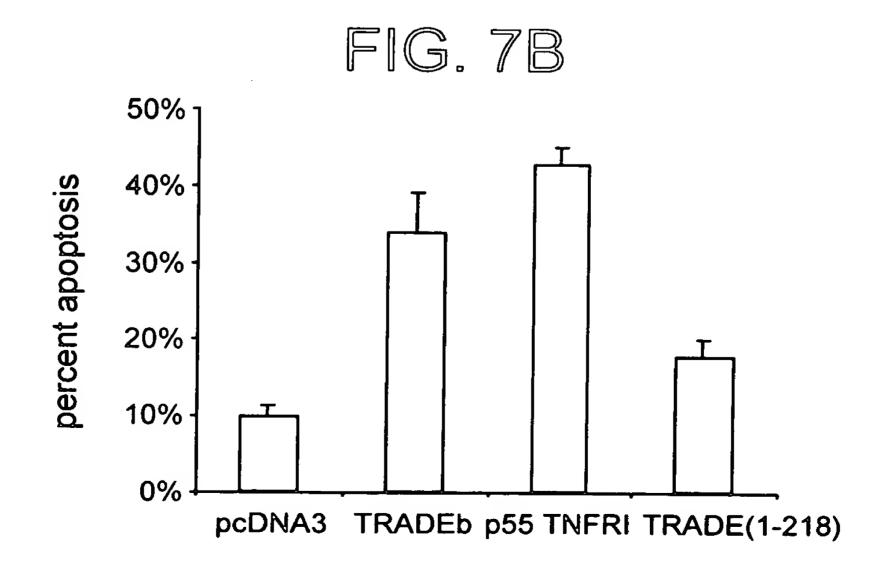
FIG. 6B

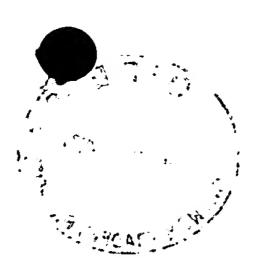


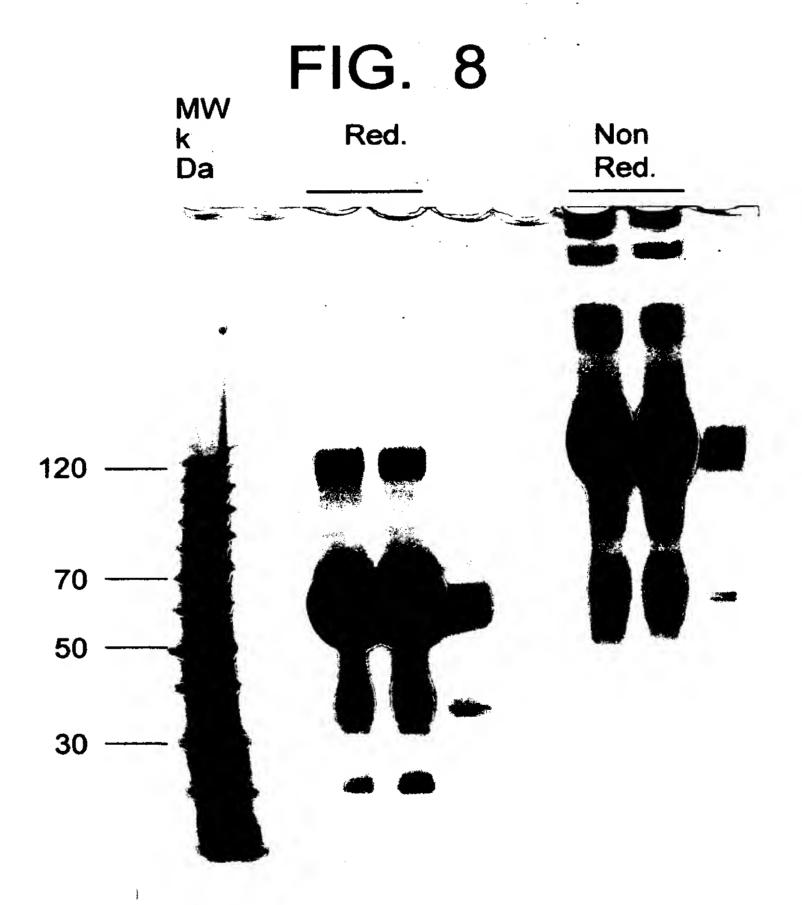
CLASS SUBCLASS

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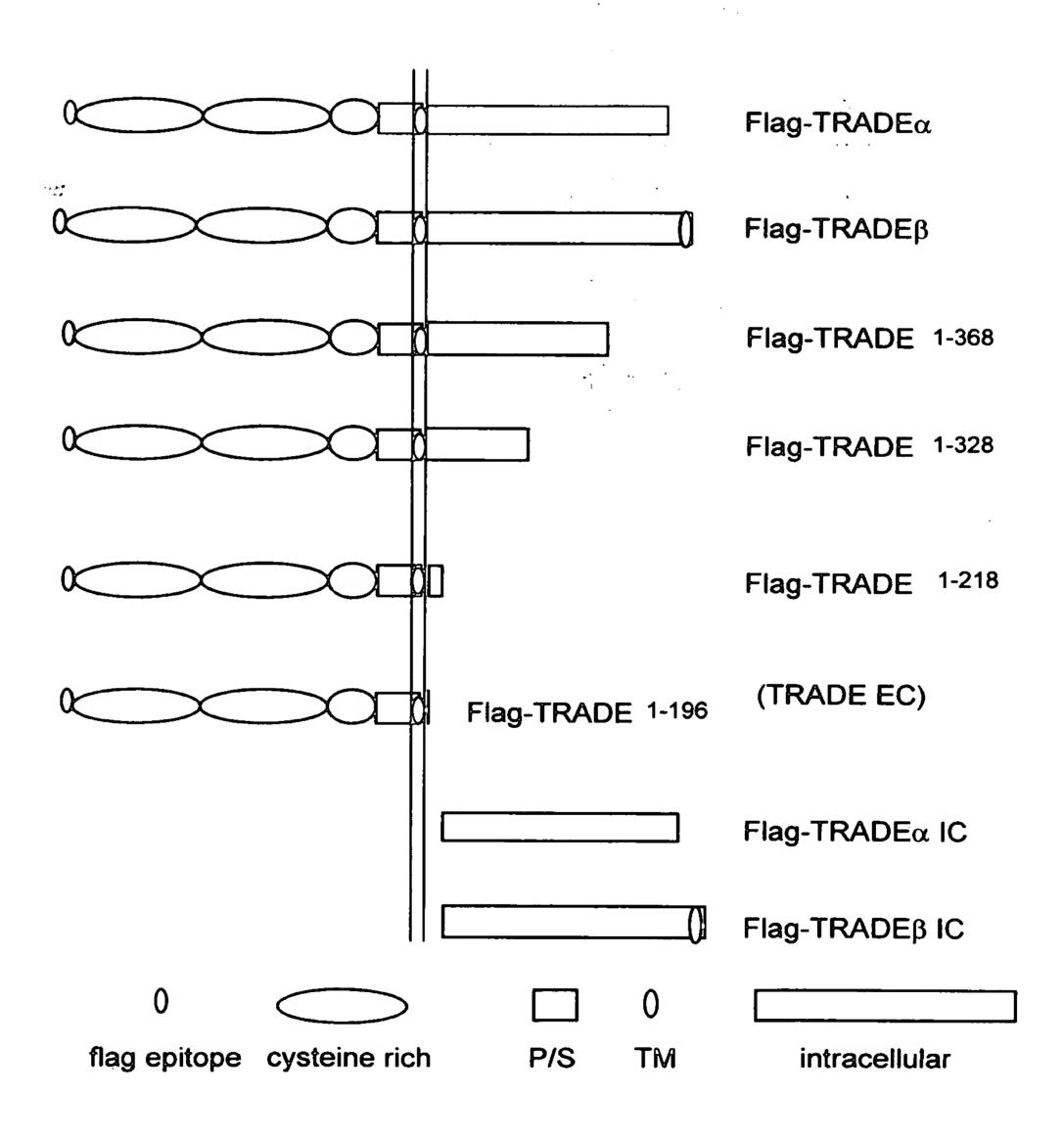




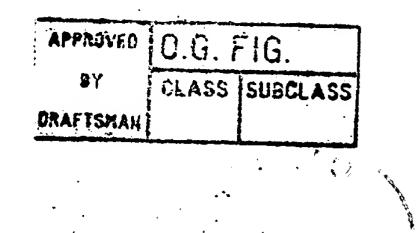
CLASS SUBCLASS

DRAFTSMAH

FIG. 9

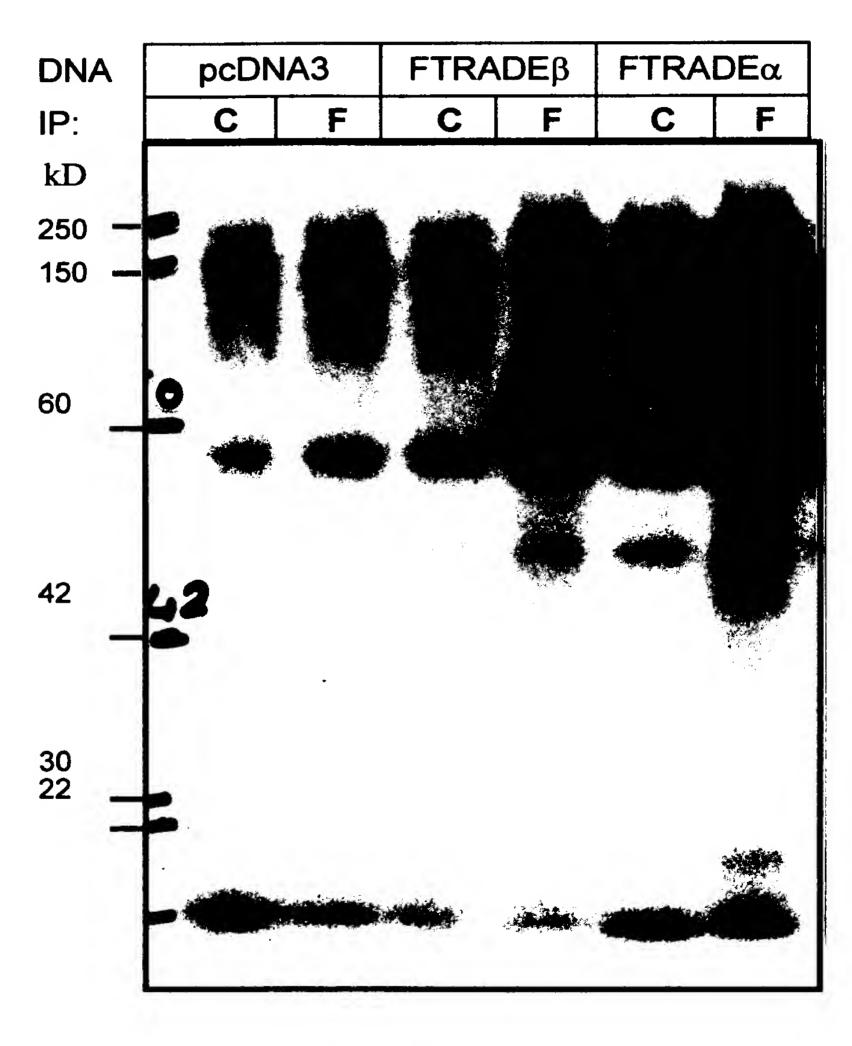


Deletion analysis



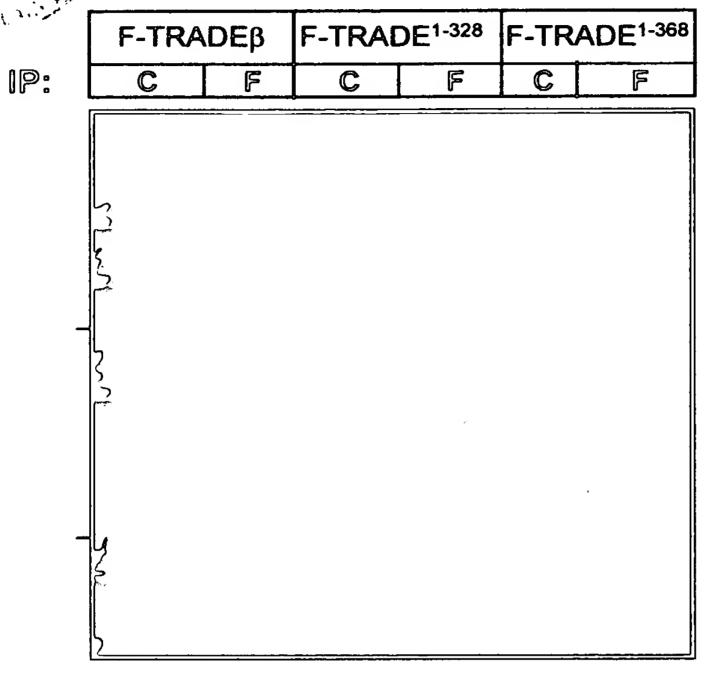
÷:

FIG. 10



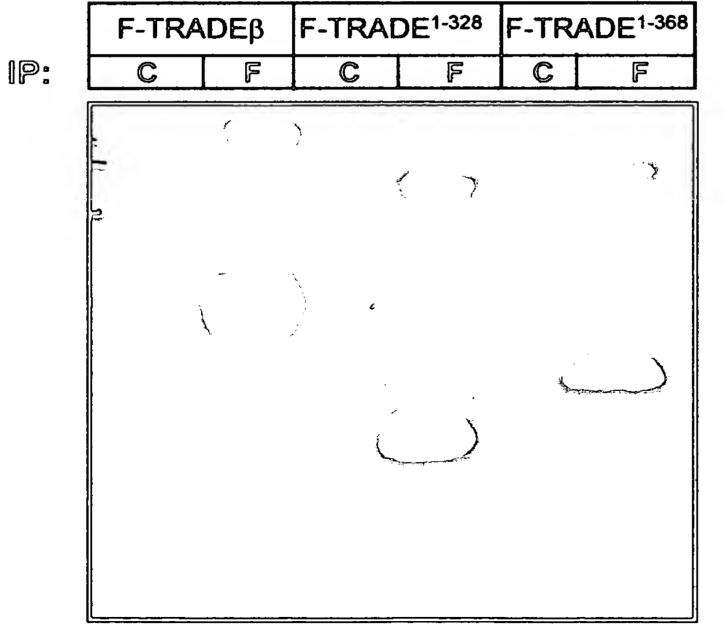
THE THE THE THE TANK THE THE THE THE THE THE THE THE THE





Kinase assay

FIG. 11B



anti-Flag blot

The first that the first than that there



$HA-TRAF6(\Delta N) +$

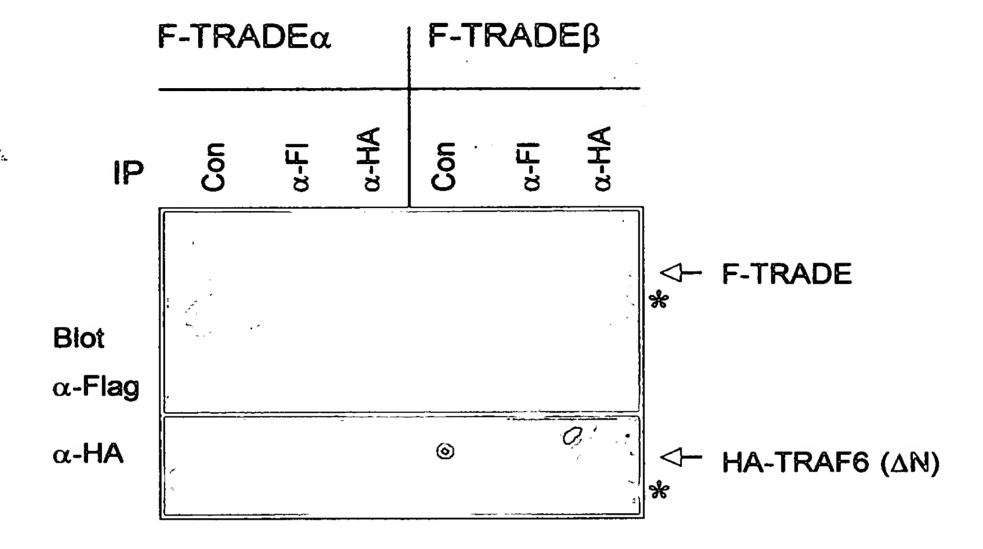
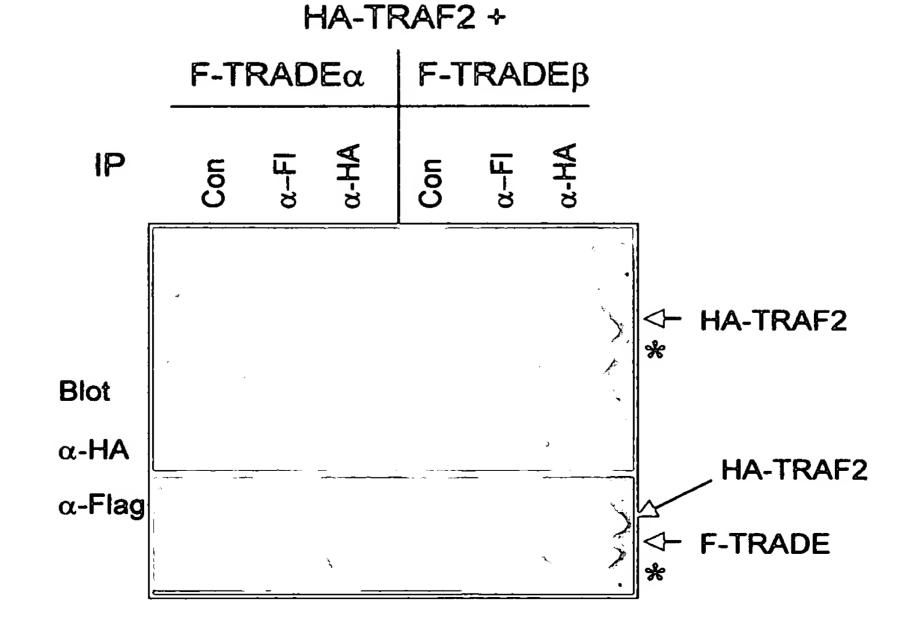
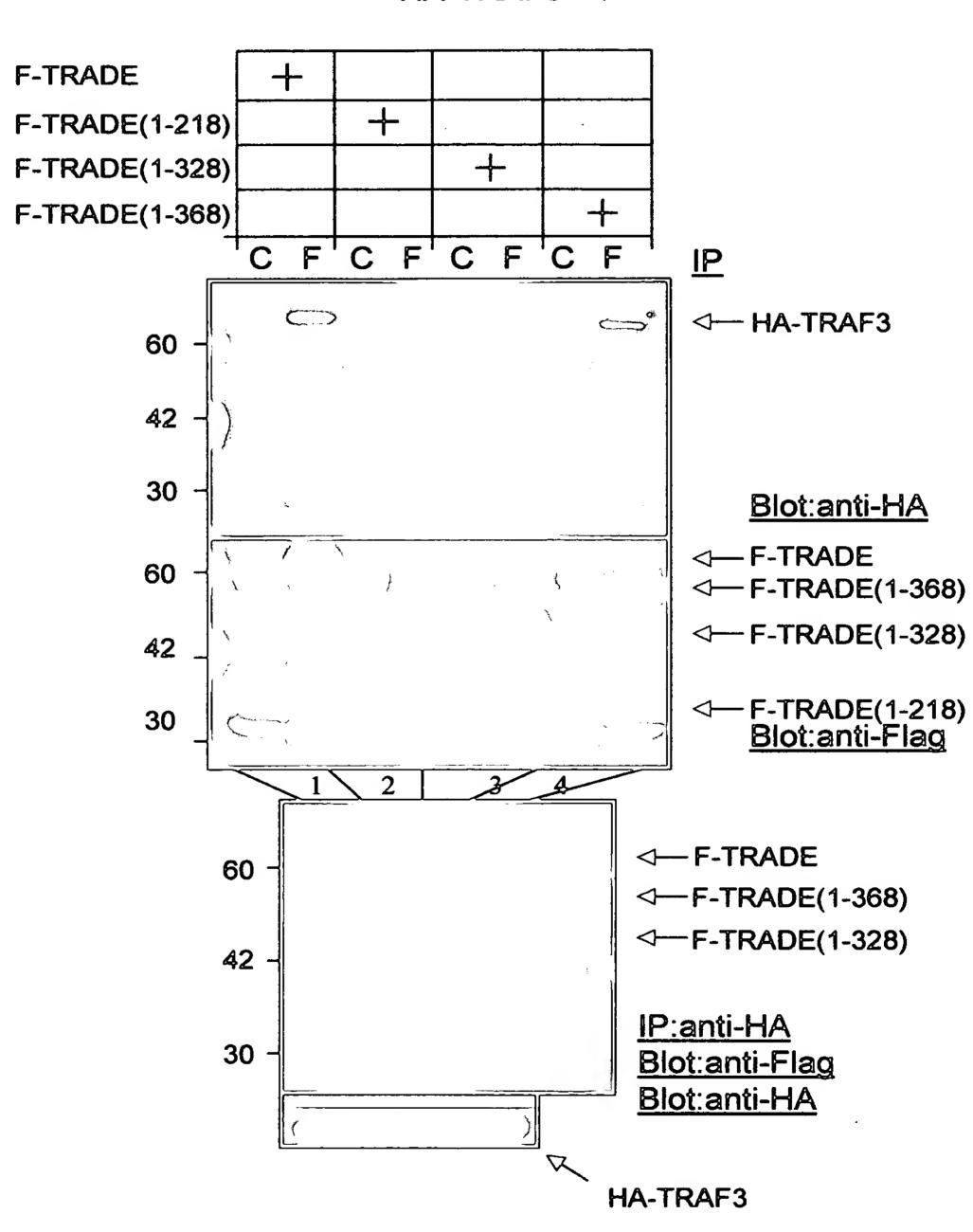


FIG. 12B





HA-TRAF3+



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